SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method

<130> 2601WOOP

<150> JP 10-374454

<151> 1998-12-28

<150> JP 11-122688

<151> 1999-04-28

<150> JP 11-249300

<151> 1999-09-02

<160> 24

<210> 1

<211> 16

<212> PRT

<213> Rat

Sub a'

<223> The 7th cystein residue binds with the 16th cystein residue to form a intra-molecular disulfide-bond.

<400> 1

Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys
1   5   10   15

<210> 2

<211> 19

<212> PRT

<213> Rat

<223> The 7th cystein residue binds with the 16th cystein residue to form a intra-molecular disulfide-bond.

<400> 2

Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys
1 5 10 15

Trp Gln Val
19

<210> 3

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 3

GTCGACATGG ATCTGCAAAC CTCGTTGCTG TG 32

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

Sub a' cont

<223>

<400> 4

ACTAGTTCAG GTGCCTTTGC TTTCTGTCCT CT 32

<210> 5

<211> 353

<212> PRT

<213> Rat

<400> 5

Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn
1 5 10 15

Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
20 25 30
Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45
Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
50 55 60
Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
65 70 75 80
Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
85 90 95
Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110
Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
115 120 125
Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
130 135 140
Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
145 150 155 160
Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
165 170 175
Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
180 185 190
Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
195 200 205
Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
210 215 220
Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala

Sub a1 cont

225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg

245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr

260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr

275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser

290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys

305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr

325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly

340 345 350

Thr

<210> 6

<211> 1074

<212> DNA

<213> Rat

<400> 6

Sub a1 cont

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ATCAACATCA TTATGCCTTC CGTGTTTGGT ACCATCTGTC TCCTGGGCAT CGTGGGAAAC 180

TCCACGGTCA TCTTTGCTGT GGTGAAGAAG TCCAAGCTAC ACTGGTGCAG CAACGTCCCC 240

GACATCTTCA TCATCAACCT CTCTGTGGTG GATCTGCTCT TCCTGCTGGG CATGCCTTTC 300

ATGATCCACC AGCTCATGGG GAACGGCGTC TGGCACTTTG GGGAAACCAT GTGCACCCTC 360

ATCACAGCCA TGGACGCCAA CAGTCAGTTC ACTAGCACCT ACATCCTGAC TGCCATGACC 420
ATTGACCGCT ACTTGGCCAC CGTCCACCCC ATCTCCTCCA CCAAGTTCCG GAAGCCCTCC 480
ATGGCCACCC TGGTGATCTG CCTCCTGTGG GCGCTCTCCT TCATCAGTAT CACCCCTGTG 540
TGGCTCTACG CCAGGCTCAT TCCCTTCCCA GGGGGTGCTG TGGGCTGTGG CATCCGCCTG 600
CCAAACCCGG ACACTGACCT CTACTGGTTC ACTCTGTACC AGTTTTTCCT GGCCTTTGCC 660
CTTCCGTTTG TGGTCATTAC CGCCGCATAC GTGAAAATAC TACAGCGCAT GACGTCTTCG 720
GTGGCCCCAG CCTCCCAACG CAGCATCCGG CTTCGGACAA AGAGGGTGAC CCGCACGGCC 780
ATTGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT GCAGCTGACC 840
CAGCTGTCCA TCAGCCGCCC GACCCTCACG TTTGTCTACT TGTACAACGC GGCCATCAGC 900
TTGGGCTATG CTAACAGCTG CCTGAACCCC TTTGTGTACA TAGTGCTCTG TGAGACCTTT 960
CGAAAACGCT TGGTGTTGTC AGTGAAGCCT GCAGCCCAGG GGCAGCTCCG CACGGTCAGC 1020
AACGCTCAGA CAGCTGATGA GGAGAGGACA GAAAGCAAAG GCACCTGAAC TAGT 1074

<210> 7

<211> 326

<212> RNA

<213> Rat

<400> 7

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AUCAGCUGUC UGAGCGUUGC UGACCGUGCG GAGCUGCCCC UGGGCUGCAG GCUUCACUGA 180
CAACACCAAG CGUUUUCGAA AGGUCUCACA GAGCACUAUG UACACAAAGG GGUUCAGGCA 240
GCUGUUAGCA UAGCCCAAGC UG 262

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

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<223>

<400> 8

CAACAGCTGC CTCAACCC 18

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<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 9

CCTGGTGATC TGCCTCCT 18

<210> 10

<211> 1275

<212> DNA

<213> Human

<400> 10

Sub a' cont

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GGACAAGGTG GCAGGCGCTG GAGGCTGCCG CAGCCTGCGT GGGTGGAGGG GAGCTCAGCT 180
CGGTTGTGGG AGCAGGCGAC CGGCACTGGC TGGATGGACC TGGAAGCCTC GCTGCTGCCC 240
ACTGGTCCCA ACGCCAGCAA CACCTCTGAT GGCCCCGATA ACCTCACTTC GGCAGGATCA 300
CCTCCTCGCA CGGGGAGCAT CTCCTACATC AACATCATCA TGCCTTCGGT GTTCGGCACC 360
ATCTGCCTCC TGGGCATCAT CGGGAACTCC ACGGTCATCT TCGCGGTCGT GAAGAAGTCC 420
AAGCTGCACT GGTGCAACAA CGTCCCCGAC ATCTTCATCA TCAACCTCTC GGTAGTAGAT 480
CTCCTCTTTC TCCTGGGCAT GCCCTTCATG ATCCACCAGC TCATGGGCAA TGGGGTGTGG 540
CACTTTGGGG AGACCATGTG CACCCTCATC ACGGCCATGG ATGCCAATAG TCAGTTCACC 600
AGCACCTACA TCCTGACCGC CATGGCCATT GACCGCTACC TGGCCACTGT CCACCCCATC 660

TCTTCCACGA AGTTCCGGAA GCCCTCTGTG GCCACCCTGG TGATCTGCCT CCTGTGGGCC 720

CTCTCCTTCA TCAGCATCAC CCCTGTGTGG CTGTATGCCA GACTCATCCC CTTCCCAGGA 780

GGTGCAGTGG GCTGCGGCAT ACGCCTGCCC AACCCAGACA CTGACCTCTA CTGGTTCACC 840

CTGTACCAGT TTTTCCTGGC CTTTGCCCTG CCTTTTGTGG TCATCACAGC CGCATACGTG 900

AGGATCCTGC AGCGCATGAC GTCCTCAGTG GCCCCCGCCT CCCAGCGCAG CATCCGGCTG 960

CGGACAAAGA GGGTGACCCG CACAGCCATC GCCATCTGTC TGGTCTTCTT TGTGTGCTGG 1020

GCACCCTACT ATGTGCTACA GCTGACCCAG TTGTCCATCA GCCGCCCGAC CCTCACCTTT 1080

GTCTACTTAT ACAATGCGGC CATCAGCTTG GGCTATGCCA ACAGCTGCCT CAACCCCTTT 1140

GTGTACATCG TGCTCTGTGA GACGTTCCGC AAACGCTTGG TCCTGTCGGT GAAGCCTGCA 1200

GCCCAGGGGC AGCTTCGCGC TGTCAGCAAC GCTCAGACGG CTGACGAGGA GAGGACAGAA 1260

AGCAAAGGCA CCTGA 1275

<210> 11

<211> 422

<212> PRT

<213> Human

<400> 11

MeT Ser Val Gly Ala MeT Lys Lys Gly Val Gly Arg Ala Val Gly Leu

1 5 10 15

Sub a1 cont

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20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro

35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala

50 55 60

Thr Gly Thr Gly Trp MeT Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly

65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile MeT

100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser

115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn

130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu

145 150 155 160

Phe Leu Leu Gly MeT Pro Phe MeT Ile His Gln Leu MeT Gly Asn Gly

165 170 175

Val Trp His Phe Gly Glu Thr MeT Cys Thr Leu Ile Thr Ala MeT Asp

180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala MeT Ala Ile

195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg

210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser

225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe

245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr

260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu

275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg MeT

290 295 300

Sub a1 cont

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320
Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335
Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350
Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365
Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380
Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400
Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415
Thr Glu Ser Lys Gly Thr
420

Sub a1 cont

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<210> 13
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<213> Artificial Sequence

<220>

<223>

<400> 13

ACTAGTTCAG GTGCCTTTGC TTTCTGTCCT C 31

<210> 14

<211> 33

<212> DNA

<213> Artificial Sequence

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<223>

<400> 14

AGTCGACATG TCAGTGGGAG CCATGAAGAA GGG 33

<210> 15

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223>

Sub a1 cont

<400> 15

AACTAGTTCA GGTGCCTTTG CTTTCTGTCC TCT 33

<210> 16

<211> 1074

<212> DNA

<213> Human

<400> 16

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ATCAACATCA TCATGCCTTC GGTGTTCGGC ACCATCTGCC TCCTGGGCAT CATCGGGAAC 180
TCCACGGTCA TCTTCGCGGT CGTGAAGAAG TCCAAGCTGC ACTGGTGCAA CAACGTCCCC 240
GACATCTTCA TCATCAACCT CTCGGTAGTA GATCTCCTCT TTCTCCTGGG CATGCCCTTC 300
ATGATCCACC AGCTCATGGG CAATGGGGTG TGGCACTTTG GGGAGACCAT GTGCACCCTC 360
ATCACGGCCA TGGATGCCAA TAGTCAGTTC ACCAGCACCT ACATCCTGAC CGCCATGGCC 420
ATTGACCGCT ACCTGGCCAC TGTCCACCCC ATCTCTTCCA CGAAGTTCCG GAAGCCCTCT 480
GTGGCCACCC TGGTGATCTG CCTCCTGTGG GCCCTCTCCT TCATCAGCAT CACCCCTGTG 540
TGGCTGTATG CCAGACTCAT CCCCTTCCCA GGAGGTGCAG TGGGCTGCGG CATACGCCTG 600
CCCAACCCAG ACACTGACCT CTACTGGTTC ACCCTGTACC AGTTTTTCCT GGCCTTTGCC 660
CTGCCTTTTG TGGTCATCAC AGCCGCATAC GTGAGGATCC TGCAGCGCAT GACGTCCTCA 720
GTGGCCCCCG CCTCCCAGCG CAGCATCCGG CTGCGGACAA AGAGGGTGAC CCGCACAGCC 780
ATCGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT ACAGCTGACC 840
CAGTTGTCCA TCAGCCGCCC GACCCTCACC TTTGTCTACT TATACAATGC GGCCATCAGC 900
TTGGGCTATG CCAACAGCTG CCTCAACCCC TTTGTGTACA TCGTGCTCTG TGAGACGTTC 960
CGCAAACGCT TGGTCCTGTC GGTGAAGCCT GCAGCCCAGG GGCAGCTTCG CGCTGTCAGC 1020
AACGCTCAGA CGGCTGACGA GGAGAGGACA GAAAGCAAAG GCACCTGAAC TAGT 1074

<210> 17

<211> 1283

<212> DNA

<213> Human

<400> 17

Sub a1 cont

AGTCGACATG TCAGTGGGAG CCATGAAGAA GGGAGTGGGG AGGGCAGTTG GGCTTGGAGG 60
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GGGACAAGGT GGCAGGCGCT GGAGGCTGCC GCAGCCTGCG TGGGTGGAGG GGAGCTCAGC 180
TCGGTTGTGG GAGCAGGCGA CCGGCACTGG CTGGATGGAC CTGGAAGCCT CGCTGCTGCC 240
CACTGGTCCC AACGCCAGCA ACACCTCTGA TGGCCCCGAT AACCTCACTT CGGCAGGATC 300

ACCTCCTCGC ACGGGGAGCA TCTCCTACAT CAACATCATC ATGCCTTCGG TGTTCGGCAC 360
CATCTGCCTC CTGGGCATCA TCGGGAACTC CACGGTCATC TTCGCGGTCG TGAAGAAGTC 420
CAAGCTGCAC TGGTGCAACA ACGTCCCCGA CATCTTCATC ATCAACCTCT CGGTAGTAGA 480
TCTCCTCTTT CTCCTGGGCA TGCCCTTCAT GATCCACCAG CTCATGGGCA ATGGGGTGTG 540
GCACTTTGGG GAGACCATGT GCACCCTCAT CACGGCCATG GATGCCAATA GTCAGTTCAC 600
CAGCACCTAC ATCCTGACCG CCATGGCCAT TGACCGCTAC CTGGCCACTG TCCACCCCAT 660
CTCTTCCACG AAGTTCCGGA AGCCCTCTGT GGCCACCCTG GTGATCTGCC TCCTGTGGGC 720
CCTCTCCTTC ATCAGCATCA CCCCTGTGTG GCTGTATGCC AGACTCATCC CCTTCCCAGG 780
AGGTGCAGTG GGCTGCGGCA TACGCCTGCC CAACCCAGAC ACTGACCTCT ACTGGTTCAC 840
CCTGTACCAG TTTTTCCTGG CCTTTGCCCT GCCTTTTGTG GTCATCACAG CCGCATACGT 900
GAGGATCCTG CAGCGCATGA CGTCCTCAGT GGCCCCCGCC TCCCAGCGCA GCATCCGGCT 960
GCGGACAAAG AGGGTGACCC GCACAGCCAT CGCCATCTGT CTGGTCTTCT TTGTGTGCTG 1020
GGCACCCTAC TATGTGCTAC AGCTGACCCA GTTGTCCATC AGCCGCCCGA CCCTCACCTT 1080
TGTCTACTTA TACAATGCGG CCATCAGCTT GGGCTATGCC AACAGCTGCC TCAACCCCTT 1140
TGTGTACATC GTGCTCTGTG AGACGTTCCG CAAACGCTTG GTCCTGTCGG TGAAGCCTGC 1200
AGCCCAGGGG CAGCTTCGCG CTGTCAGCAA CGCTCAGACG GCTGACGAGG AGAGGACAGA 1260
AAGCAAAGGC ACCTGAACTA GTT 1283

<210> 18

Sub a1 cont

<211> 420

<212> RNA

<213> Human

<400> 18

CAAAAGCUGG AGCUCCACCG CGGUGGCGGC CGCUCUAGCC CACUAGUUCA GGUGCCUUUG 60
CUUUCUGUCC UCUCCUCGUC AGCCGUCUGA GCGUUGCUGA CAGCGCGAAG CUGCCCCUGG 120
GCUGCAGGCU UCACCGACAG GACCAAGCGU UUGCGGAACG UCUCACAGAG CACGAUGUAC 180
ACAAAGGGGU UGAGGCAGCU GUUGGCAUAG CCCAAGCUGA UGGCCGCAUU GUAUAAGUAG 240
ACAAAGGUGA GGGUCGGGCG GCUGAUGGAC AACUGGGUCA GCUGUAGCAC AUAGUAGGGU 300

GCCCAGCACA CAAAGAAGAC CAGACAGAUG GCGAUGGCUG UGCGGGUCAC CCUCUUUGUC 360

CGCAGCCGGA UGCUGCGCUG GGAGGCGGGG GCCACUGAGG ACGUCAUGCG CUGCAGGAUC 420

<210> 19

<211> 18

<212> PRT

<213> Rat

<223> The 6th cystein residue binds with the 15th cystein residue to form a intra-molecular disulfide-bond.

<400> 19

Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp
1 5 10 15

Gln Val
18

<210> 20

<211> 17

<212> PRT

<213> Rat

<223> The 5th cystein residue binds with the 14th cystein residue to form a intra-molecular disulfide-bond.

Sub a! cont

<400> 20

Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln
1 5 10 15

Val
17

<210> 21

<211> 16

<212> PRT

<213> Rat

<223> The 4th cystein residue binds with the 13th cystein residue to form a intra-molecular disulfide-bond.

<400> 21

Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val
1 5 10 15 16

<210> 22

<211> 15

<212> PRT

<213> Rat

<223> The 3rd cystein residue binds with the 12th cystein residue to form a intra-molecular disulfide-bond.

<400> 22

Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val
1 5 10 15

<210> 23

<211> 14

<212> PRT

<213> Rat

Sue a1 cnt

<223> The 2nd cystein residue binds with the 11th cystein residue to form a intra-molecular disulfide-bond.

<400> 23

Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val
1 5 10

<210> 24

<211> 13

<212> PRT

<213> Rat

<223> The 1st cystein residue binds with the 10th cystein residue to form a intra-molecular disulfide-bond.

<400> 24

Cys Met Leu Gly Arg Val Tyr Arg Pro Cys Trp Gln Val
1 5 10